RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/553,305A
Source: IFW P
Date Processed by STIC: 11/3/06

ENTERED

IFWP

RAW SEQUENCE LISTING DATE: 11/03/2006
PATENT APPLICATION: **US/10/553,305A** TIME: 10:29:04

Input Set : **A:\64312465.APP**
Output Set: **N:\CRF4\11032006\J553305A.raw**

```
 3 <110> APPLICANT: KOBAYASHI, NORIHIRO
 4       GODA, YASUHIRO
 5       HIROBE, MASATO
 7 <120> TITLE OF INVENTION: PROTEIN CAPABLE OF BINDING PLASTICIZER
 9 <130> FILE REFERENCE: 64312(46590)
11 <140> CURRENT APPLICATION NUMBER: 10/553,305A
12 <141> CURRENT FILING DATE: 2005-10-14
14 <150> PRIOR APPLICATION NUMBER: PCT/JP04/005250
15 <151> PRIOR FILING DATE: 2004-04-13
17 <150> PRIOR APPLICATION NUMBER: JP 2003-110877
18 <151> PRIOR FILING DATE: 2003-04-15
20 <160> NUMBER OF SEQ ID NOS: 34
22 <170> SOFTWARE: PatentIn version 3.3
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 363
26 <212> TYPE: DNA
27 <213> ORGANISM: Mus musculus
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(363)
34 <400> SEQUENCE: 1
35 gag gtg cat ctg gtg gag tct ggg gga gac tta gtg agg cct gga ggg       48
36 Glu Val His Leu Val Glu Ser Gly Gly Asp Leu Val Arg Pro Gly Gly
37 1               5                   10                  15
39 tcc ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc gga agt tat       96
40 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ser Tyr
41             20                  25                  30
43 ggc atg tct tgg gtt cgc cag act gca gac aag agg ctg gag tgg gtc      144
44 Gly Met Ser Trp Val Arg Gln Thr Ala Asp Lys Arg Leu Glu Trp Val
45         35                  40                  45
47 gca acc att tat agt ggt ggt ttt tac acc tac tat cca gac agt gtg      192
48 Ala Thr Ile Tyr Ser Gly Gly Phe Tyr Thr Tyr Tyr Pro Asp Ser Val
49     50                  55                  60
51 agg gga cga ttc acc atc tcc aga gac aat gtc aag gaa atc gtg tat      240
52 Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Lys Glu Ile Val Tyr
53 65                  70                  75                  80
55 ctg caa atg agc agt ctg aag tct gag gac aca gcc atg tat tac tgt      288
56 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
57                 85                  90                  95
59 gca aga cgg acg gta gta tct acg gac tat act ttg gac tac tgg ggt      336
60 Ala Arg Arg Thr Val Val Ser Thr Asp Tyr Thr Leu Asp Tyr Trp Gly
61             100                 105                 110
63 caa gga acc tca gtc atc gtc tcc tca                                 363
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64 Gln Gly Thr Ser Val Ile Val Ser Ser
65         115                 120
68 <210> SEQ ID NO: 2
69 <211> LENGTH: 121
70 <212> TYPE: PRT
71 <213> ORGANISM: Mus musculus
73 <400> SEQUENCE: 2
74 Glu Val His Leu Val Glu Ser Gly Gly Asp Leu Val Arg Pro Gly Gly
75 1               5                  10                  15
78 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Ser Tyr
79             20                  25                  30
82 Gly Met Ser Trp Val Arg Gln Thr Ala Asp Lys Arg Leu Glu Trp Val
83         35                  40                  45
86 Ala Thr Ile Tyr Ser Gly Gly Phe Tyr Thr Tyr Tyr Pro Asp Ser Val
87     50                  55                  60
90 Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Val Lys Glu Ile Val Tyr
91 65                  70                  75                  80
94 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
95                 85                  90                  95
98 Ala Arg Arg Thr Val Val Ser Thr Asp Tyr Thr Leu Asp Tyr Trp Gly
99             100                 105                 110
102 Gln Gly Thr Ser Val Ile Val Ser Ser
103         115                 120
106 <210> SEQ ID NO: 3
107 <211> LENGTH: 318
108 <212> TYPE: DNA
109 <213> ORGANISM: Mus musculus
112 <220> FEATURE:
113 <221> NAME/KEY: CDS
114 <222> LOCATION: (1)..(318)
116 <400> SEQUENCE: 3
117 gat atc cag ata aca cag att aca tcc tcc ctg gct gcc tct ctg gga      48
118 Asp Ile Gln Ile Thr Gln Ile Thr Ser Ser Leu Ala Ala Ser Leu Gly
119 1               5                  10                  15
121 gac aga gtc acc atc agt tgc cgg cca agt cag gac atc agc aat ttt      96
122 Asp Arg Val Thr Ile Ser Cys Arg Pro Ser Gln Asp Ile Ser Asn Phe
123             20                  25                  30
125 tta aac tgg ttt cag cag aaa cca gat gga act gtt gaa gtc ctg atc     144
126 Leu Asn Trp Phe Gln Gln Lys Pro Asp Gly Thr Val Glu Val Leu Ile
127         35                  40                  45
129 tgc tac aca tta aga atg cac tta gga gtc cca tca acg ttc agt ggc     192
130 Cys Tyr Thr Leu Arg Met His Leu Gly Val Pro Ser Thr Phe Ser Gly
131     50                  55                  60
133 tgt gtg tct gga aca tat tat act ctc acc agt agc aac ctg gaa caa     240
134 Cys Val Ser Gly Thr Tyr Tyr Thr Leu Thr Ser Ser Asn Leu Glu Gln
135 65                  70                  75                  80
137 gaa gat ata gac act tcc ttt gcc att agg att ata cgc gtg ctc acg     288
138 Glu Asp Ile Asp Thr Ser Phe Ala Ile Arg Ile Ile Arg Val Leu Thr
139                 85                  90                  95
```

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```
141 gtc ggt gca ggg acc acg ctg gag ctg aaa                                 318
142 Val Gly Ala Gly Thr Thr Leu Glu Leu Lys
143             100                 105
146 <210> SEQ ID NO: 4
147 <211> LENGTH: 106
148 <212> TYPE: PRT
149 <213> ORGANISM: Mus musculus
151 <400> SEQUENCE: 4
152 Asp Ile Gln Ile Thr Gln Ile Thr Ser Ser Leu Ala Ala Ser Leu Gly
153 1               5                   10                  15
156 Asp Arg Val Thr Ile Ser Cys Arg Pro Ser Gln Asp Ile Ser Asn Phe
157             20                  25                  30
160 Leu Asn Trp Phe Gln Gln Lys Pro Asp Gly Thr Val Glu Val Leu Ile
161         35                  40                  45
164 Cys Tyr Thr Leu Arg Met His Leu Gly Val Pro Ser Thr Phe Ser Gly
165     50                  55                  60
168 Cys Val Ser Gly Thr Tyr Tyr Thr Leu Thr Ser Ser Asn Leu Glu Gln
169 65                  70                  75                  80
172 Gln Asp Ile Asp Thr Ser Phe Ala Ile Arg Ile Ile Arg Val Leu Thr
173                 85                  90                  95
176 Val Gly Ala Gly Thr Thr Leu Glu Leu Lys
177             100                 105
180 <210> SEQ ID NO: 5
181 <211> LENGTH: 15
182 <212> TYPE: PRT
183 <213> ORGANISM: Artificial Sequence
185 <220> FEATURE:
186 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
187       linker
189 <400> SEQUENCE: 5
190 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
191 1               5                   10                  15
194 <210> SEQ ID NO: 6
195 <211> LENGTH: 14
196 <212> TYPE: PRT
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
201       linker
203 <400> SEQUENCE: 6
204 Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Lys Gly
205 1               5                   10
208 <210> SEQ ID NO: 7
209 <211> LENGTH: 18
210 <212> TYPE: PRT
211 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
215       linker
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PATENT APPLICATION: **US/10/553,305A** TIME: 10:29:04

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217 <400> SEQUENCE: 7
218 Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Ser Gly Ser Thr
219 1               5                   10                  15
222 Lys Gly
226 <210> SEQ ID NO: 8
227 <211> LENGTH: 12
228 <212> TYPE: PRT
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
233       linker
235 <400> SEQUENCE: 8
236 Gly Ser Thr Ser Gly Lys Pro Ser Glu Gly Lys Gly
237 1               5                   10
240 <210> SEQ ID NO: 9
241 <211> LENGTH: 18
242 <212> TYPE: PRT
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
247       linker
249 <400> SEQUENCE: 9
250 Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
251 1               5                   10                  15
254 Lys Gly
258 <210> SEQ ID NO: 10
259 <211> LENGTH: 18
260 <212> TYPE: DNA
261 <213> ORGANISM: Artificial Sequence
263 <220> FEATURE:
264 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
265       primer
267 <400> SEQUENCE: 10
268 gcttgccggg tgggccac                                              18
271 <210> SEQ ID NO: 11
272 <211> LENGTH: 18
273 <212> TYPE: DNA
274 <213> ORGANISM: Artificial Sequence
276 <220> FEATURE:
277 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
278       primer
280 <400> SEQUENCE: 11
281 acactgctgg acagggat                                              18
284 <210> SEQ ID NO: 12
285 <211> LENGTH: 28
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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RAW SEQUENCE LISTING DATE: 11/03/2006
PATENT APPLICATION: **US/10/553,305A** TIME: 10:29:04

Input Set : **A:\64312465.APP**
Output Set: **N:\CRF4\11032006\J553305A.raw**

```
291       primer
293 <400> SEQUENCE: 12
294 ggatcccggg agtacccctt gaccaggc                                    28
297 <210> SEQ ID NO: 13
298 <211> LENGTH: 18
299 <212> TYPE: DNA
300 <213> ORGANISM: Artificial Sequence
302 <220> FEATURE:
303 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
304       primer
306 <400> SEQUENCE: 13
307 gttgaagctc ttgacaat                                               18
310 <210> SEQ ID NO: 14
311 <211> LENGTH: 27
312 <212> TYPE: DNA
313 <213> ORGANISM: Artificial Sequence
315 <220> FEATURE:
316 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
317       primer
319 <400> SEQUENCE: 14
320 ggatcccggg tggatggtgg gaagatg                                     27
323 <210> SEQ ID NO: 15
324 <211> LENGTH: 36
325 <212> TYPE: DNA
326 <213> ORGANISM: Artificial Sequence
328 <220> FEATURE:
329 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
330       primer
332 <220> FEATURE:
333 <221> NAME/KEY: modified_base
334 <222> LOCATION: (24)
335 <223> OTHER INFORMATION: inosine
337 <220> FEATURE:
338 <221> NAME/KEY: modified_base
339 <222> LOCATION: (25)
340 <223> OTHER INFORMATION: inosine
342 <220> FEATURE:
343 <221> NAME/KEY: modified_base
344 <222> LOCATION: (29)
345 <223> OTHER INFORMATION: inosine
347 <220> FEATURE:
348 <221> NAME/KEY: modified_base
349 <222> LOCATION: (30)
350 <223> OTHER INFORMATION: inosine
352 <220> FEATURE:
353 <221> NAME/KEY: modified_base
354 <222> LOCATION: (34)
355 <223> OTHER INFORMATION: inosine
357 <220> FEATURE:
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/03/2006
PATENT APPLICATION: **US/10/553,305A** TIME: 10:29:06

Input Set : **A:\64312465.APP**
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; N Pos. 24,25,29,30,34,35

VERIFICATION SUMMARY DATE: 11/03/2006
PATENT APPLICATION: **US/10/553,305A** TIME: 10:29:06

Input Set : **A:\64312465.APP**
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L:363 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0